

RESULT 1

ALDX\_SPOSA

ID ALDX\_SPOSA STANDARD; PRT; 322 AA.  
AC P27800; Q12707;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Aldehyde reductase I (EC 1.1.1.2) (Alcohol dehydrogenase [NADP+])  
DE (ALR).  
GN ARI.  
OS Sporobolomyces salmonicolor.  
OC Eukaryota; Fungi; Basidiomycota; Urediniomycetes;  
OC Microbotryomycetidae; Sporidiobolales; Sporidiobolus.  
OX NCBI\_TaxID=5005;  
RN [1]  
RP SEQUENCE FROM N.A., SEQUENCE OF 33-124; 132-153; 156-199 AND  
RP 202-313, AND FUNCTION.  
RC STRAIN=Aku 4429;  
RX MEDLINE=96271678; PubMed=8779568;  
RA Kita K., Matsuzaki K., Hashimoto T., Yanase H., Kato N.,  
RA Chung M.C.-M., Kataoka M., Shimizu S.;  
RT "Cloning of the aldehyde reductase gene from a red yeast,  
RT Sporobolomyces salmonicolor, and characterization of the gene and its  
RT product.";  
RL Appl. Environ. Microbiol. 62:2303-2310(1996).  
RN [2]  
RP SEQUENCE OF 1-51, AND ENZYME REGULATION.  
RC STRAIN=Aku 4429;  
RX MEDLINE=92338224; PubMed=1633196;  
RA Kataoka M., Sakai H., Morikawa T., Katoh M., Miyoshi T., Shimizu S.,  
RA Yamada H.;  
RT "Characterization of aldehyde reductase of Sporobolomyces  
RT salmonicolor.";  
RL Biochim. Biophys. Acta 1122:57-62(1992).  
CC -!- FUNCTION: Catalyzes the asymmetric reduction of aliphatic and  
CC aromatic aldehydes and ketones to an R-enantiomer. Reduces ethyl  
CC 4-chloro-3-oxobutanoate to ethyl (R)-4-chloro-3-hydroxybutanoate.  
CC -!- CATALYTIC ACTIVITY: An alcohol + NADP(+) = an aldehyde + NADPH.  
CC -!- ENZYME REGULATION: Inhibited by quercetin, dicoumarol and some SH-  
CC reagents.  
CC -!- SUBUNIT: Monomer.  
CC -!- SIMILARITY: Belongs to the aldo/keto reductase family.  
CC -----  
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CC -----  
DR EMBL; U26463; AAB17362.1; -.  
DR PIR; S78113; S78113.  
DR HSSP; P15121; 2ACQ.  
DR GO; GO:0005623; C:cell; IDA.  
DR GO; GO:0008106; F:alcohol dehydrogenase (NADP) activity; IDA.  
DR InterPro; IPR001395; Aldo/ket\_red.

DR Pfam; PF00248; aldo\_ket\_red; 1.  
 DR PRINTS; PR00069; ALDKETRDTASE.  
 DR ProDom; PD000288; Aldo/ket\_red; 1.  
 DR PROSITE; PS00798; ALDOKETO\_REDUCTASE\_1; FALSE\_NEG.  
 DR PROSITE; PS00062; ALDOKETO\_REDUCTASE\_2; 1.  
 DR PROSITE; PS00063; ALDOKETO\_REDUCTASE\_3; FALSE\_NEG.  
 KW Oxidoreductase; NADP.  
 FT INIT\_MET 0 0  
 FT ACT\_SITE 48 48 HYDROGEN-BOND DONOR (BY SIMILARITY).  
 SQ SEQUENCE 322 AA; 35208 MW; 418A824DF5352DE1 CRC64;

Query Match 54.2%; Score 925; DB 1; Length 322;  
 Best Local Similarity 57.4%; Pred. No. 4.4e-61;  
 Matches 186; Conservative 38; Mismatches 84; Indels 16; Gaps 4;

Qy	9 LNDGNSIPALGYGTWQAEPGVQVGEVKLAVKAGYRHLDLAKVYQNQTEIGQALKELFDEG 68
	: :             :      : ::                    :     :
Db	6 LNTGASLELVGYGTWQAAPGEVGQGVKVAIETGYRHLDLAKVYSNQPEVGAAIK---EA 61
Qy	69 VVKREDLFITSKLWNNRHAPEHVEPALDETLKELGLSYLDLYLIHWPVAFKFPPDE--- 125
	:
Db	62 GVKREDLFITSKLWNNSHRPEQVEPALDDTLKELGLEYLDLYLIHWPVAF---PPEGDI 117
Qy	126 ---LLPADPTNKDLAYIDDSVKLSDTWKAVVALKKTGKTKSVGSNFSTRLVDLVEEASG 182
	:               :              :      :     :     :
Db	118 TQNLFP--KANDKEVKLDLEVSLVDTWKAMVKLLDTGKVKAIGVSNFDAKIMVDAIEATG 175
Qy	183 ERPAVNQIEAHPLLQQDELVAHHKSKNIVITAYSPLGNVAGKPPLTENPGIVDAAKRLN 242
	:                :                           :                   :
Db	176 VTPSVNQIERHPLLLQPELIAHHKAKNIHITAYSPLGNNTVGAPLLVQHPEIKRIAEKNG 235
Qy	243 HTPAAVLIAWGIQRGYSVLKVSVTPSRIRKSNSFEQITLSDEEFQRVTNLIKEYESRNVP 302
	:     :            :   :                             :
Db	236 CTPAQVLIAWAIVGGHSVIPKSVTPSRIGENFKQVSLSQEDVDAVSKLGEGSGRRRYNIP 295
Qy	303 FNYKPSWSIDVFGTQYEAKATHKI 326
	:     :     :     :
Db	296 CTYSPKWIDINVFGEEDEKSCKNAV 319

RESULT 2

US-10-040-416-6

; Sequence 6, Application US/10040416  
; Publication No. US20020160480A1  
; GENERAL INFORMATION:  
; APPLICANT: OOKURA, TETUYA  
; APPLICANT: KASUMI, TAKAFUMI  
; APPLICANT: ASABA, EIJI  
; TITLE OF INVENTION: ERYTHROSE REDUCTASE, ITS cDNA AND CELL WHICH THE cDNA  
EXPRESS  
; FILE REFERENCE: 217969US0XCIP  
; CURRENT APPLICATION NUMBER: US/10/040,416  
; CURRENT FILING DATE: 2002-01-09  
; PRIOR APPLICATION NUMBER: US 09/800,487  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: JP 2001-001294  
; PRIOR FILING DATE: 2001-01-09  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 328  
; TYPE: PRT  
; ORGANISM: Trichosporonoides megachiliensis

US-10-040-416-6

Query Match 99.4%; Score 1697; DB 13; Length 328;  
Best Local Similarity 99.4%; Pred. No. 2.8e-156;  
Matches 326; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSYNKNIPLNDGNSIPALGYGTWQAEPGVGEGVKLAVKAGYRHLDLAKVYQNQTEIGQA 60  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 1 MSYNKNIPLNDGNSIPALGYGTWQAEPGVGEGVKLAVKAGYRHLDLAKVYQNQTEIGQA 60  
  
Qy 61 LKELFDEGVVKREDLFITSKLWNNRHAPEHVEPALDETLKELGLSYLDLYLIHWPVAFKF 120  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 61 LKELFDEGVVKREDLFITSKLWNNRHAPEHVEPALDETLKELGLSYLDLYLIHWPVAFKF 120  
  
Qy 121 TTPDELLPADPTNKDLAYIDDSVKLSDTWKAVVALKKTGKTKSVGSNFSTRVLVDLVEEA 180  
||| ||| ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 121 TTPDELLPADPTNKDLAYVDDSVKLSDTWKAVVALKKTGKTKSVGSNFSTRVLVDLVEEA 180  
  
Qy 181 SGERPAVNQIEAHPLLQQDELVAHHKSKNIVITAYSPLGNVAGKPPLTENPGIVDAAKR 240  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 181 SGERPAVNQIEAHPLLQQDELVAHHKSKNIVITAYSPLGNVAGKPPLTENPGIVDAAKR 240  
  
Qy 241 LNHTPAAVLIAWGIQRGYSVLVKSVTPSRIKSNEQITLSDEEFQRTNLKEYGESRNN 300  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 241 LNHTPAAVLIAWGIQRGYSVLVKSVTPSRIKSNEQITLSDEEFQRTNLKEYGESRNN 300  
  
Qy 301 VPFNYKPSWSIDVFGTQYEAKATHKINA 328  
||| ||| ||| ||| ||| ||| |||  
Db 301 VPFNYKPSWSIDVFGTQDEAKATHKINA 328



Qy 243 HTPAAVLIAWGIQRGYSVLVKSVTPEKSNFEQITLSDEEFQRVTNLIKEYGESRNNVP 302  
||| ||||| | |:||: ||||||| ||:||:|| |: | : | | | :|  
Db 237 CTPAQVLIAWAIVGGSVIPKSVTPSRIGENFKQVSLSQEDVDAVSKLGEGRSGRRYNIP 296

Qy 303 FNYKPSWSIDVFGTQYEAKATHKI 326  
| | | | :||| : | : :  
Db 297 CTYSPKWIDINVFGEEDEKSCKNAV 320